AMENDMENTS TO THE SPECIFICATION

At page 1, after the title, "Promoter for the epidermis-specific transgenic expression in plants," please insert the following section heading:

CROSS-REFERENCE TO RELATED APPLICATIONS

At page 1 in the application as originally filed, prior to the first paragraph, please insert the following section headings and phrases:

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

Not Applicable

INCORPORATION-BY-REFERENCE OF MATERIAL SUBMITTED ON A COMPACT DISC

Not Applicable

BACKGROUND OF THE INVENTION

Field of the Invention

At page 1 in the application as originally filed, after the first paragraph, please insert the following section heading:

Description of Related Art

At page 3 in the application as originally filed, after the first full paragraph, please insert the following section heading:

BRIEF SUMMARY OF THE INVENTION

At page 4 in the application as originally filed, after the first paragraph, please insert the following section heading:

DETAILED DESCRIPTION OF THE INVENTION

At page 8, please amend the second full paragraph as follows:

Sequence identities are conventionally determined via different alignment programs, like for example CLUSTAL. In general, the person skilled in the art has at his disposal suitable algorithms for determining the sequence identity~~, for example also the program, which is~~

~~accessible under http://www.ncbi.nlm.nih.gov/BLAST (for example the link „standard nucleotide-nucleotide BLAST [blastn]“).~~

At page 16 in the application as originally filed, after the second paragraph, please insert the following section heading:

BRIEF DESCRIPTION OF THE DRAWINGS

Please amend the paragraph spanning pages 19-20 as follows:

pPS3:

With the adaptor primers 5‘ ATA TAT CTG CAG GGA GCC ACG GCC GTC CAC (SEQ ID No. 10) and 5‘ TAT CCC GGG CCC GTG CCT GGA CGG GAA (SEQ ID No. 11), a PCR fragment of about 240 bp was generated and its ends were cut with *Sma*I and *Pst*I (via Adaptor). The genomic WIR1a clone served as PCR template. The PCR fragment contained the last 15 amino acids of the first exon of WIR1a and the intron including splice site acceptor, and was ligated in pPS1, cut with *Pst*I (partially) and *Sma*I and purified by means of agarose gel electrophoresis. The resulting construct contained a translational WIR1a::GUS fusion with the WIR1 intron before the GUS gene. Furthermore, a deletion of amino acids Nos. 18 - 35 of the first exon of WIR1a was introduced in order to prevent the secretion of the WIR1a::GUS fusion protein (by means of removing the signal peptide).

At page 20, please amend the first full paragraph as follows:

pPS15:

The WIR1a promoter was replaced by a PCR fragment of the GSTA1 promoter. To this end, pPS3 was (partially) digested with *Xho*I and *Sna*BI and the vector band was purified by means of agarose gel electrophoresis. The GSTA1 promoter fragment of about 2.3 kb length was amplified by means of PCR with the adaptor primers 5‘ATA TAT CTC GAG TCT AGA ACT AGT GGA TCC (SEQ ID No. 12) and 5‘ATA TAT TAC GTA GTT TGT CCG TGA ACT TCA (SEQ ID No. 13) from the genomic GSTA1 clone and cut at the ends with *Xho*I und *Sna*BI. The PCR fragment was ligated with the gel-eluated pPS3 band, resulting in a translational fusion of the intron-containing WIR1a gene fragment with GUS under the control of the GSTA1 promoter.

At page 20, please amend the second full paragraph as follows:
pPS18:

pPS15 was (partially) digested with *Pst*I and *Sna*BI, the vector band was purified by means of agarose gel electrophoresis and ligated with a double-stranded oligonucleotide (5'GTA CAC AGG CAG CTA GCT CTC GAA ACC TCG CTC GAA ACG CA (SEQ ID No. 14) plus 5'CAT GTG TCC GTC GAT CGA GAG CTT TGG AGC GAG CTT TGC GT (SEQ ID No. 15)). This replaced the part of the WIR1a gene located around the translation start (46 bp upstream to 53 bp downstream of the translation start) with 42 bp of the 5'UTR of the WIR1a gene without the translation initiation codon ATG. The resulting construct contained a transcriptional fusion of the intron-containing WIR1a gene fragment with GUS under the control of the GSTA1 promoter.

Please amend the paragraph spanning pages 21-22 as follows:

From this construct, the *Mla1* intron together with a part of the coding sequence of the *TaMlo1* gene was isolated as an about 1.55 kb *Pst*I/*Msc*I fragment (= fragment 1). Parallel to this, a fragment of about 450 bp was amplified by means of PCR from the plasmid pBSw41 with the oligonucleotides T3 (standard sequencing primer for pBluescript) and TaMlo1-1 (5′ GTC GCA TGC CTG TCC ACA CGA AAT GTG C 3′ (SEQ ID No. 16), *Sph*I, restriction site underlined). Subsequently, the PCR fragment was digested by means of the restriction enzymes *Pst*I and *Sph*I (= fragment 2). The vector pPS24 (promoter + oxalate oxidase, see above) was opened by means of restriction digestion with *Sma*I and *Sph*I and the oxalate oxidase gene fragment, which was cut out, was discarded. Thereupon, the above-described fragments 1 and 2 were ligated into the *Sma*I/*Sph*I-cut vector pPS24 in a three-component ligation. In this ligation, the ends of the *Msc*I and *Sma*I-cut components are compatible, as both are so-called blunt ends. The resulting construct (pTaMlo1 RNAi) contains about 300 bp of the *TaMlo1* gene as well as about 150 bp polylinker/adaptor sequence as „inverted repeats", separated by the *Mla1* intron. The control of this transcription unit is subject to the GSTA1 promoter.